

Kip3A

864 aa full length sequence

The motor domain is amino acids **5**–**348** or base pair **143**–**1174**.

```
5      GCGGCCGCGAATTCGGCACCAGGGGCGCTCTCTCCCGGTGTGGGTACTGCTGTCTGTGGT      60
      1  -----+-----+-----+-----+-----+-----+
10     GTGGCTGTGGGACCCGTGAGCAAGCAGCGACGCCAGCGGCGGAGAACCGACGAAAGGTGT      120
      61  -----+-----+-----+-----+-----+-----+
15     CACCACAGTGATGGCAGTGGAGGACAGCACGCTGCAAGTAGTGGTACGGGTGCGGCCCCC      180
      121 -----+-----+-----+-----+-----+-----+
           MetAlaValGluAspSerThrLeuGlnValValValArgValArgProPr
20     CACCCCTCGGGAGCTGGACAGTCAGCGGCGGCCAGTGGTTCAGGTGGTGGACGAGCGGGT      240
      181 -----+-----+-----+-----+-----+-----+
           oThrProArgGluLeuAspSerGlnArgArgProValValGlnValValAspGluArgVa
25     GCTGGTGTTTAACCCTGAGGAGCCCGATGGAGGGTTCCCTGGCCTGAAATGGGGTGGCAC      300
      241 -----+-----+-----+-----+-----+-----+
           lLeuValPheAsnProGluGluProAspGlyGlyPheProGlyLeuLysTrpGlyGlyTh
30     CCATGATGGCCCCAAGAAGAAGGGCAAAGACCTGACGTTTGTCTTTGACCGGGTCTTTGG      360
      301 -----+-----+-----+-----+-----+-----+
           rHisAspGlyProLysLysLysGlyLysAspLeuThrPheValPheAspArgValPheGl
35     CGAGGCGGCCACCCAACAGGACGTGTTCCAGCACACCACGCACAGCGTCCTGGACAGCTT      420
      361 -----+-----+-----+-----+-----+-----+
           yGluAlaAlaThrGlnGlnAspValPheGlnHisThrThrHisSerValLeuAspSerPh
40     CCTCCAGGGCTACAACCTGCTCAGTGTTCCTACGGGGCCACCGGGGCTGGGAAGACACA      480
      421 -----+-----+-----+-----+-----+-----+
           eLeuGlnGlyTyrAsnCysSerValPheAlaTyrGlyAlaThrGlyAlaGlyLysThrHi
45     CACCATGCTGGGAAGGGAGGGGACCCCGGCATCATGTACCTGACCACCGTGGAACTGTA      540
      481 -----+-----+-----+-----+-----+-----+
           sThrMetLeuGlyArgGluGlyAspProGlyIleMetTyrLeuThrThrValGluLeuTy
50     CAGGCGCCTGGAGGCCCGCCAGCAGAGAAGCACTTCGAGGTGCTCATCAGCTACCAGGA      600
      541 -----+-----+-----+-----+-----+-----+
           rArgArgLeuGluAlaArgGlnGlnGluLysHisPheGluValLeuIleSerTyrGlnGl
```

Fig. 1A

5	601	GGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGGCCCCTTGCCATCCGCGA -----+-----+-----+-----+-----+-----+-----+ uValTyrAsnGluGlnIleHisAspLeuLeuGluProLysGlyProLeuAlaIleArgG1	660
	661	GGACCCCGACAAGGGGGTGGTGGTGAAGGACTTTCTTTCCACCAGCCAGCCTCAGCCGA -----+-----+-----+-----+-----+-----+-----+ uAspProAspLysGlyValValValGlnGlyLeuSerPheHisGlnProAlaSerAlaG1	720
10	721	GCAGCTGCTGGAGATACTGACCAGGGGAACCGTAACCGCACGCAGCACCCCACTGATGC -----+-----+-----+-----+-----+-----+-----+ uGlnLeuLeuGluIleLeuThrArgGlyAsnArgAsnArgThrGlnHisProThrAspAl	780
15	781	CAACGCGACTTCCTCCCGCTCCCATGCCATCTTCCAGATCTTGTGAAGCAGCAGGACCG -----+-----+-----+-----+-----+-----+-----+ aAsnAlaThrSerSerArgSerHisAlaIlePheGlnIlePheValLysGlnGlnAspAr	840
20	841	GGTTCAGGACTGACCCAGGCTGTCCAGGTGGCCAAGATGAGCCTGATTGACCTGGCTGG -----+-----+-----+-----+-----+-----+-----+ gValProGlyLeuThrGlnAlaValGlnValAlaLysMetSerLeuIleAspLeuAlaG1	900
25	901	CTCAGAGCGGGCATCCAGCACCCATGCGAAGGGGGAGCGGCTGCGGGAGGGGGCCAACAT -----+-----+-----+-----+-----+-----+-----+ ySerGluArgAlaSerSerThrHisAlaLysGlyGluArgLeuArgGluGlyAlaAsnIl	960
30	961	CAACCGCTCTCTGCTGGCGCTCATCAACGTCCTCAATGCCTTGCCCGATGCAAAGGGCCG -----+-----+-----+-----+-----+-----+-----+ eAsnArgSerLeuLeuAlaLeuIleAsnValLeuAsnAlaLeuAlaAspAlaLysGlyAr	1020
35	1021	CAAGACCCATGTGCCCTACCGGGACAGCAAAGTACCCGCCTGCTCAAAGACTCCCTCGG -----+-----+-----+-----+-----+-----+-----+ gLysThrHisValProTyrArgAspSerLysLeuThrArgLeuLeuLysAspSerLeuG1	1080
40	1081	GGGCAACTGCCGCACAGTGATGATCGCTGCCATCAGCCCCTCCAGCCTGACCTACGAGGA -----+-----+-----+-----+-----+-----+-----+ yGlyAsnCysArgThrValMetIleAlaAlaIleSerProSerSerLeuThrTyrGluAs	1140
45	1141	CACGTACAACACCCTCAAATATGCCGACCGG <b>GCC</b> AAGGAGATCAGGCTCTCGCTGAAGAG -----+-----+-----+-----+-----+-----+-----+ pThrTyrAsnThrLeuLysTyrAlaAspArg <b>Ala</b> LysGluIleArgLeuSerLeuLysSe	1200
50	1201	CAATGTGACCAGCCTGGACTGTCACATCAGCCAGTATGCTACCATCTGCCAACAGCTCCA -----+-----+-----+-----+-----+-----+-----+ rAsnValThrSerLeuAspCysHisIleSerGlnTyrAlaThrIleCysGlnGlnLeuG1	1260

Fig. 1B

5  
1261 GGCTGAGGTAGCCGCTCTGAGGAAGAAGCTCCAAGTGTATGAGGGGGGAGGCCAGCCCCC 1320  
-----+-----+-----+-----+-----+  
nAlaGluValAlaAlaLeuArgLysLysLeuGlnValTyrGluGlyGlyGlyGlnProPr

10  
1321 ACCACAGGACCTCCCAGGATCTCCCAAGTCGGGACCACCACCAGAACACCTTCCCAGCTC 1380  
-----+-----+-----+-----+-----+  
oProGlnAspLeuProGlySerProLysSerGlyProProProGluHisLeuProSerSe

15  
1381 CCCCTTGCCACCCACCCCTCCCAGCCAGCCCTGCACCCCAGAGCTCCCTGCAGGGCCTAG 1440  
-----+-----+-----+-----+-----+  
rProLeuProProHisProProSerGlnProCysThrProGluLeuProAlaGlyProAr

20  
1441 AGCCCTTCAAGAGGAGAGTCTGGGGATGGAGGCCAGGTGGAGAGGGCCATGGAAGGGAA 1500  
-----+-----+-----+-----+-----+  
gAlaLeuGlnGluGluSerLeuGlyMetGluAlaGlnValGluArgAlaMetGluGlyAs

25  
1501 CTCTTCAGACCAGGAGCAGTCCCCAGAGGATGAGGATGAAGGCCAGCTGAGGAGGTTCC 1560  
-----+-----+-----+-----+-----+  
nSerSerAspGlnGluGlnSerProGluAspGluAspGluGlyProAlaGluGluValPr

30  
1561 AACCCAGATGCCAGAGCAGAACCCACACATGCACTGCCAGAGTCCCCTCGCCTGACCCCT 1620  
-----+-----+-----+-----+-----+  
oThrGlnMetProGluGlnAsnProThrHisAlaLeuProGluSerProArgLeuThrLe

35  
1621 GCAGCCCCAAGCCAGTCGTGGGCCACTTCTCAGCACGGGAACTGGATGGGGACCGTTCTAA 1680  
-----+-----+-----+-----+-----+  
uGlnProLysProValValGlyHisPheSerAlaArgGluLeuAspGlyAspArgSerLy

40  
1681 GCAGTTGGCCCTAAAGGTGCTGTGCGTTGCCAGCGGCAGTACTCCCTGCTCCAAGCAGC 1740  
-----+-----+-----+-----+-----+  
sGlnLeuAlaLeuLysValLeuCysValAlaGlnArgGlnTyrSerLeuLeuGlnAlaAl

45  
1741 CAACCTCCTGACGCCCCGACATGATCACAGAGTTTGAGACCCTACAGCAGCTGGTGCAAGA 1800  
-----+-----+-----+-----+-----+  
aAsnLeuLeuThrProAspMetIleThrGluPheGluThrLeuGlnGlnLeuValGlnGl

50  
1801 GGAAAAAATTGAGCCTGGGGCAGAGGCCTTGAGGACTTCAGGCCTGGCCAGGGGGGCACC 1860  
-----+-----+-----+-----+-----+  
uGluLysIleGluProGlyAlaGluAlaLeuArgThrSerGlyLeuAlaArgGlyAlaPr

55  
1861 TCTGGCTCAGGAGCTGTGTTTCAGAGTCAATCCCTGTGCCGTCTCCTCTCTGCCAGAGCC 1920  
-----+-----+-----+-----+-----+  
oLeuAlaGlnGluLeuCysSerGluSerIleProValProSerProLeuCysProGluPr

Fig. 1C

1921 TCCAGGATACACTGGCCCTGTGACCCGGACTATGGCGAGGCGACTGAGTGGCCCCCTGCA 1980  
-----+-----+-----+-----+-----+  
oProGlyTyrThrGlyProValThrArgThrMetAlaArgArgLeuSerGlyProLeuHi

1981 CACCCTGGGAATCCCGCCTGGACCCAACTGCACCCAGCCCAGGGGTCCCGATGGCCCAT 2040  
-----+-----+-----+-----+-----+  
sThrLeuGlyIleProProGlyProAsnCysThrProAlaGlnGlySerArgTrpProMe

2041 GGAGAAGAAGAGGAGGAGACCAAGCGCCTTGGAGGCAGACAGTCCCATGGCCTCAAAGCG 2100  
-----+-----+-----+-----+-----+  
tGluLysLysArgArgArgProSerAlaLeuGluAlaAspSerProMetAlaSerLysAr

2101 GGGACCAAGCGCCAGCGCCAGTCCTTCCTGCCCTGCCTAAGGAGAGGGTCTCTGCCTGA 2160  
-----+-----+-----+-----+-----+  
gGlyThrLysArgGlnArgGlnSerPheLeuProCysLeuArgArgGlySerLeuProAs

2161 CACCCAACCTTCACAGGGGCCAGCACCCCCAAAGGAGAAAGGGCCTCCTCCCCCTGCCA 2220  
-----+-----+-----+-----+-----+  
pThrGlnProSerGlnGlyProSerThrProLysGlyGluArgAlaSerSerProCysHi

2221 TTCCCCTCGCGTTTGCCAGCCACAGTCATCAAAGCCGGGTGCCCTGGGCCCTTCCGC 2280  
-----+-----+-----+-----+-----+  
sSerProArgValCysProAlaThrValIleLysSerArgValProLeuGlyProSerAl

2281 CATGCAGAACTGCTCCACCCCGCTGGCTCTGCCCACTCGAGACCTCAATGCCACCTTTGA 2340  
-----+-----+-----+-----+-----+  
aMetGlnAsnCysSerThrProLeuAlaLeuProThrArgAspLeuAsnAlaThrPheAs

2341 TCTCTCTGAGGAGCTCCCTCAAAGCCCAGTTTCCATGAATGCATTGGCTGGGACAAAAT 2400  
-----+-----+-----+-----+-----+  
pLeuSerGluGluProProSerLysProSerPheHisGluCysIleGlyTrpAspLysIl

2401 ACCCCAGGAGCTGAGCAGGCTGGACCAGCCCTTCATCCCCAGGGCACCTGTGCCCTGTT 2460  
-----+-----+-----+-----+-----+  
eProGlnGluLeuSerArgLeuAspGlnProPheIleProArgAlaProValProLeuPh

2461 CACCATGAAGGGCCCCAAGCCAACATCTTCCCTCCCTGGGACCTCTGCCTGCAAGAAGAA 2520  
-----+-----+-----+-----+-----+  
eThrMetLysGlyProLysProThrSerSerLeuProGlyThrSerAlaCysLysLysLy

2521 GCGCGTTGCGAGTTCCTCAGTCTCCCATGGCCGCAGCCGCATCGCCCGCTCCCCAGCAG 2580  
-----+-----+-----+-----+-----+  
sArgValAlaSerSerSerValSerHisGlyArgSerArgIleAlaArgLeuProSerSe

Fig. 1D

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2581 CACTTTGAAGAGGCCAGCTGGGCCCCCTGTACTCCCAGAGCTGCCCTTGAGTCCCCTGTG  
-----+-----+-----+-----+-----+ 2640  
rThrLeuLysArgProAlaGlyProLeuValLeuProGluLeuProLeuSerProLeuCy

2641 CCCTAGCAACCGGAGGAATGGAAGGACCTCATCAGGGTGGGAGAGCGCTCTCAGCAGG  
-----+-----+-----+-----+-----+ 2700  
sProSerAsnArgArgAsnGlyLysAspLeuIleArgValGlyArgAlaLeuSerAlaGl

2701 GAACGGCGTCACCAAGGTGTCCTGACCGCCAGAATGTCTTGACCACCAAGGTGTCCTAAC  
-----+-----+-----+-----+-----+ 2760  
yAsnGlyValThrLysValSer

2761 CTACCGGCCCCCTCTGCTGGATACCCCTCTTGGACCTGTAGCCACCTGCACCAGGAGCTGG  
-----+-----+-----+-----+-----+ 2820

2821 ACCTGCCTTCCTTACCTGGGAGCAATTAGTGCCAACACACCTTTGCTGTATTAACATCCC  
-----+-----+-----+-----+-----+ 2880

2881 TCCCCAGACATCCATCCTGCTACTCACCTCTGTTAATCTCCTGTTAACTCAGCTTCTT  
-----+-----+-----+-----+-----+ 2940

2941 GGCATGTACATATTTCATTTGTGAGTGTAAATGTGCTGCTGTTTTTTGTTTTTGGTGGTT  
-----+-----+-----+-----+-----+ 3000

3001 TTGTTTTTTTTGTTTTTTTGTGATGGAGTCTTACTCTGTCGCCCAGGCTGGAGTG  
-----+-----+-----+-----+-----+ 3060

3061 CAGTGGTACGATCTTGGCTCACTGCAACCTCCGCCTCCTGGGTCAAGTAATTCTCCTGC  
-----+-----+-----+-----+-----+ 3120

3121 CTCAGCTTTCCAAGTAGCTGGGATTACAGGCACCCATACCACACCCAGCTAATTTTCGT  
-----+-----+-----+-----+-----+ 3180

3181 CTTTTTAATAGAGAGGGGTTTTTCCATGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTC  
-----+-----+-----+-----+-----+ 3240

3241 AGGTGATCCGCCTGCCTCAGCTTCCCAAAGTGCTGAGATTACAGGCATGAGCTACCACGC  
-----+-----+-----+-----+-----+ 3300

3301 CTGGCCCGTGTTGCTGTTTTAAAGGTGCTGCCATGTTCCCCATCTTTTTTTTTTTGAG  
-----+-----+-----+-----+-----+ 3360

Fig. 1E

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3361 ATGGAGTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGTGGCGATCTTGGCTCACTGCA 3420  
-----+-----+-----+-----+-----+-----+  
3421 AGCTCCGCCTCCCAGGTTACACCATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTA 3480  
-----+-----+-----+-----+-----+-----+  
3481 CAGGCGCCCACCACCACGCCCAGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCAC 3540  
-----+-----+-----+-----+-----+-----+  
3541 CGTGTTAGCCAGGCTGGTCTCGATCTGACCTCATGATCCACCCGCTCGGCCTCCCAAAG 3600  
-----+-----+-----+-----+-----+-----+  
3601 TGCTGGGATTACAGGCGTGAGCCACTGCGCCCGGCCTCCCCTCTCATTTATGATGCCCTC 3660  
-----+-----+-----+-----+-----+-----+  
3661 TGTGCAGGCAGACGGCTCTTGGGCTCTTTCCCCACCTGTCTCTAACACAGGCCCCACGG 3720  
-----+-----+-----+-----+-----+-----+  
3721 TGATGGCCACAGGCAGTAGAGGAGGAATGAGGATGGGTGGGGAGCGGGAGTCGCGGCT 3780  
-----+-----+-----+-----+-----+-----+  
3781 TGGCTCTTCCTGGTTTCTGAGAGGGACATCTTCATCCCTACTCCCCTTGGTCCCCAACCA 3840  
-----+-----+-----+-----+-----+-----+  
3841 CAGTCCTGGTGAAGATGTGGATGATAATGGTGCCTTGATTCCAAATGAAGACAGCTTTA 3900  
-----+-----+-----+-----+-----+-----+  
3901 TTGCTTAACTCTATTGTACATAGGATACACGTTTCAGTGTAATAAAGTGTAAGGGGAA 3960  
-----+-----+-----+-----+-----+-----+  
3961 TTCAGGCTTAATGCTGCACCTAGATATAAATGCTAATGATACTTGGGTTTATAGCCTTCT 4020  
-----+-----+-----+-----+-----+-----+  
4021 GATCCTTTATTTCTGCATATATATATAGATATATACATATATTTTGGTATAACAATAAA 4080  
-----+-----+-----+-----+-----+-----+  
4081 CCGTCTCCATCCTTGGGAAAAAAAAAAAA 4108  
-----+-----+-----+-----+-----+-----+

Fig. 1F.

## DNA sequence of HsKIP3A, motor only

5  
10  
15  
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1 GACAGCACGC TGCAAGTAGT GGTACGGGTG CGGCCCCCA CCCCTCGGGA GCTGGACAGT  
61 CAGCGGCGGC CAGTGGTTCA GGTGGTGGAC GAGCGGGTGC TGGTGTTTAA CCCTGAGGAG  
121 CCCGATGGAG GGTCCCTGG CCTGAAATGG GGTGGCACCC ATGATGGCCC CAAGAAGAAG  
181 GGCAAAGACC TGACGTTTGT CTTTGACCGG GTCTTTGGCG AGGCGGCCAC CCAACAGGAC  
241 GTGTTCCAGC ACACCACGCA CAGCGTCCTG GACAGCTTCC TCCAGGGCTA CAACTGCTCA  
301 GTGTTTGCCT ACGGGGCCAC CGGGGCTGGG AAGACACACA CCATGCTGGG AAGGGAGGGG  
361 GACCCCGGCA TCATGTACCT GACCACCGTG GAACTGTACA GGCGCCTGGA GGCCCGCCAG  
421 CAGGAGAAGC ACTTCGAGGT GCTCATCAGC TACCAGGAGG TGTATAATGA ACAGATCCAT  
481 GACCTCCTGG AGCCCAAGGG GCCCCTTGCC ATCCGCGAGG ACCCGACAA GGGGGTGGTG  
541 GTGCAAGGAC TTTCTTTCCA CCAGCCAGCC TCAGCCGAGC AGCTGCTGGA GATACTGACC  
601 AGGGGGAACC GTAACCGCAC GCAGCACCCC ACTGATGCCA ACGCGACTTC CTCCCGCTCC  
661 CATGCCATCT TCCAGATCTT TGTGAAGCAG CAGGACCGGG TTCCAGGACT GACCCAGGCT  
721 GTCCAGGTGG CCAAGATGAG CCTGATTGAC CTGGCTGGCT CAGAGCGGGC ATCCAGCACC  
781 CATGCGAAGG GGGAGCGGCT GCGGGAGGGG GCCAACATCA ACCGCTCTCT GCTGGCGCTC  
841 ATCAACGTCC TCAATGCCTT GGCCGATGCA AAGGGCCGCA AGACCCATGT GCCCTACCGG  
901 GACAGCAAAC TGACCCGCCT GCTCAAAGAC TCCCTCGGGG GCAACTGCCG CACAGTGATG  
961 ATCGCTGCCA TCAGCCCCTC CAGCCTGACC TACGAGGACA CGTACAACAC CCTC

Fig. 2

Protein sequence of HsKIP3A, motor only

5           1   DSTLQVVVRV  RPPTPRELDS  QRRPVVQVVD  ERVLVFNPEE  PDGGFPGLKW  GGTHDGPKKK  
          61  GKDLTFVFDR  VFGEAATQOD  VFQHTTHSVL  DSFLQGYNCS  VFAYGATGAG  KTHTMLGREG  
         121  DPGIMYLTTV  ELYRRLEARQ  QEKHFVVLIS  YQEVYNEQIH  DLLEPKGPLA  IREDPDKGVV  
         181  VQGLSFHOPA  SAEQLLEILT  RGNRRRTQHP  TDANATSSRS  HAIFQIFVKQ  QDRVPGLTQA  
         241  VQVAKMSLID  LAGSERASST  HAKGERLREG  ANINRSLAL  INVLNALADA  KGRKTHVPYR  
         301  DSKLTRLLKD  SLGGNCRTVM  IAAISPSSTLT  YEDTYNTL

10   Fig. 3



Figure 4:

MAVEDSTLQVVVRVRPPTPRELDSQRRPVVQVVDERVLVFNPEEPDGGFPGLKWGGT  
HDGPKKKGKDLTFVFD RVFGAATQQDV FQHTTHSVLDSFLQGYNCSVFAYGATGAG  
KTHTMLGREGDPGIMYLT TVELYRRLEARQQEKHFEVLISYQEVYNEQI HDLLEPKG  
5 PLAIREDPDKGVVVQGLSFHQ PASAEQLLEILTRGNRNRTQHPTDANATSSRSHAI F  
QIFVKQQDRVPGLTQAVQVAKMSLIDLAGSERASSTHAKGERLREGANINRSLLALI  
NVLNALADAKGRKTHVPYRDSKLTRLLKDSLGGNCRTVMIAAISPSSTLYEDTYNTL  
KYADRAKEIRL **KGNSKLEGKPIPNPLLGLDSTRTGHHHHHH**

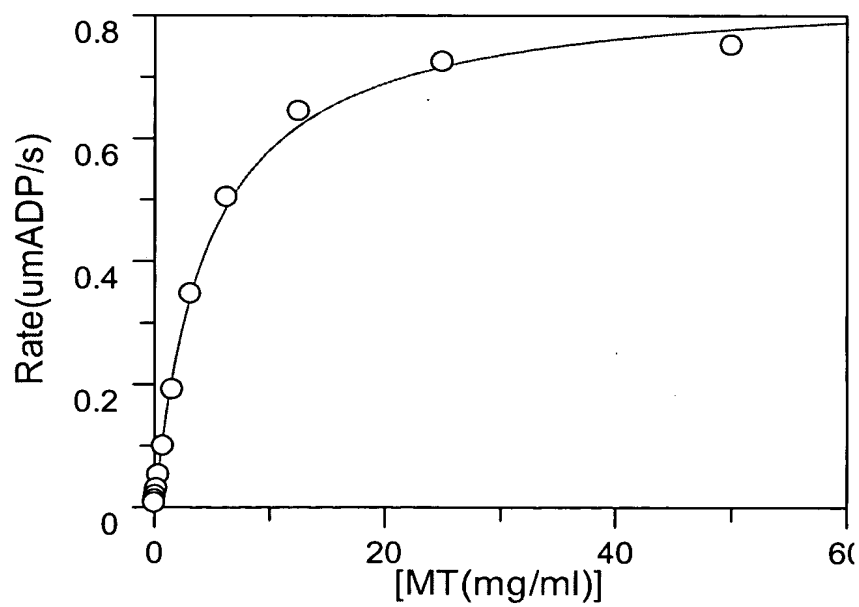
- 10     Grayed sequence is derived from the vector (pCRT7/CT, Invitrogen) and contains a V5 epitope and polyhistidine tag.

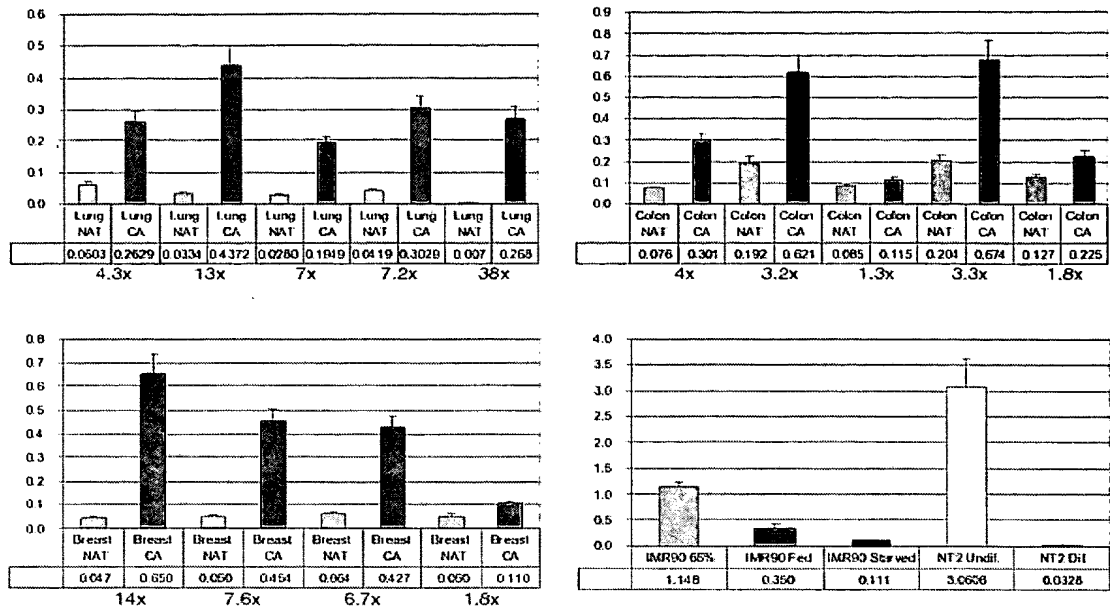
Figure 5: Nucleotide sequence of the Kip3a fragment used in the ATPase assay

ATGGCAGTGGAGGACAGCACGCTGCAAGTAGTGGTACGGGTGCGGCCCCCACCCT  
CGGGAGCTGGACAGTCAGCGGCGGCCAGTGGTTTCAGGTGGTGGACGAGCGGGTGCTG  
5 GTGTTTAACCCTGAGGAGCCCGATGGAGGGTTCCCTGGCCTGAAATGGGGTGGCACC  
CATGATGGCCCCAAGAAGAAGGGCAAAGACCTGACGTTTGTCTTTGACCGGGTCTTT  
GGCGAGGCGGCCACCCAACAGGACGTGTTCCAGCACACCACGCACAGCGTCCTGGAC  
AGCTTCCTCCAGGGCTACAACTGCTCAGTGTTCCTACGGGGCCACCGGGGCTGGG  
AAGACACACACCATGCTGGGAAGGGAGGGGGACCCGGCATCATGTACCTGACCACC  
10 GTGGAAGTGTACAGGCGCCTGGAGGCCCGCCAGCAGGAGAAGCACTTCGAGGTGCTC  
ATCAGCTACCAGGAGGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGG  
CCCCTTGCCATCCGCGAGGACCCCGACAAGGGGGTGGTGGTGCAAGGACTTTCTTTC  
CACCAGCCAGCCTCAGCCGAGCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAAC  
CGCACGCAGCACCCCACTGATGCCAACGCGACTTCCTCCCGCTCCCATGCCATCTTC  
15 CAGATCTTTGTGAAGCAGCAGGACCGGGTTCAGGACTGACCCAGGCTGTCCAGGTG  
GCCAAGATGAGCCTGATTGACCTGGCTGGCTCAGAGCGGGCATCCAGCACCCATGCG  
AAGGGGGAGCGGCTGCGGGAGGGGGCCAACATCAACCGCTCTCTGCTGGCGCTCATC  
AACGTCCTCAATGCCTTGCCGATGCAAAGGGCCGCAAGACCCATGTGCCCTACCGG  
GACAGCAAAGTACCCGCCTGCTCAAAGACTCCCTCGGGGGCAACTGCCGCACAGTG  
20 ATGATCGCTGCCATCAGCCCCTCCAGCCTGACCTACGAGGACACGTACAACACCCTC  
AAATATGCCGACCGGGCCAAGGAGATCAGGCTCAAGGGCAATTCGAAGCTTGAAGGT  
AAGCCTATCCCTAACCCTCTCCTCGGTCTCGATTCTACGCGTACCGGTCATCATCAC  
CATCACCATTGA

- 25     Grayed sequence is derived from the vector (pCRT7/CT, Invitrogen) and contains a V5 epitope and polyhistidine tag.

Fig. 6





5 Fig. 7

10 60086857 v1